

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/784,950
Source: 1FW16
Date Processed by STIC: 3/4/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/09/784,950

TIME: 15:10:41

Input Set : A:\ABXCBLCD147 CON sequence listing.txt

Output Set: N:\CRF4\03042005\I784950.raw

3 <110> APPLICANT: Davis, Geoffrey C.
 4 Blacher, Russell W.
 5 Corvalan, Jose R.
 6 Culwell, Alan R.
 7 Green, Larry L.
 8 Hales, Joanna
 9 Havrilla, Nancy
 10 Ivanov, Vladimir E.
 11 Lipani, John A.
 12 Liu, Qiang
 13 Weber, Richard F.
 14 Yang, Xiao-Dong
 15 Abgenix, Inc.

P.b

17 <120> TITLE OF INVENTION: CD147 BINDING MOLECULES AS THERAPEUTICS
 19 <130> FILE REFERENCE: ABX-CBL/CD147
 21 <140> CURRENT APPLICATION NUMBER: 09/784,950
 22 <141> CURRENT FILING DATE: 2001-02-15
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/04583
 25 <151> PRIOR FILING DATE: 1999-03-03
 27 <150> PRIOR APPLICATION NUMBER: 09/034,607
 28 <151> PRIOR FILING DATE: 1998-03-03
 30 <150> PRIOR APPLICATION NUMBER: 09/244,253
 31 <151> PRIOR FILING DATE: 1999-02-03
 33 <160> NUMBER OF SEQ ID NOS: 105
 35 <170> SOFTWARE: PatentIn Ver. 2.0
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 8
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 1
 43 Ile Thr Leu Arg Val Arg Ser His
 44 1 5
 47 <210> SEQ ID NO: 2
 48 <211> LENGTH: 7
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 2
 53 Glu Glu Arg Leu Arg Ser Tyr
 54 1 5
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 7
 59 <212> TYPE: PRT
 60 <213> ORGANISM: Homo sapiens

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62 <400> SEQUENCE: 3
63     Tyr Glu Arg Val Arg Trp Tyr
64         1             5
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 7
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 4
73     Glu Glu Arg Leu Arg Ser Tyr
74         1             5
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 7
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 5
83     Ala Glu Arg Ile Arg Ser Ile
84         1             5
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 7
89 <212> TYPE: PRT
90 <213> ORGANISM: Homo sapiens
92 <400> SEQUENCE: 6
93     Glu Glu Arg Leu Arg Ser Tyr
94         1             5
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 12
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 7
103     Thr Val His Gly Asp Leu Arg Leu Arg Ser Leu Pro
104         1             5             10
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 12
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo sapiens
112 <400> SEQUENCE: 8
113     Thr Asn Asp Ile Gly Leu Arg Gln Arg Ser His Ser
114         1             5             10
117 <210> SEQ ID NO: 9
118 <211> LENGTH: 12
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 9
123     Ser Pro Leu Leu Asp Gly Gln Arg Glu Arg Ser Tyr
124         1             5             10
127 <210> SEQ ID NO: 10
128 <211> LENGTH: 12
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens

```

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132 <400> SEQUENCE: 10
133     Tyr Asp Leu Pro Met Arg Ser Arg Ser Tyr Pro Gly
134         1             5             10
137 <210> SEQ ID NO: 11
138 <211> LENGTH: 4
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Xaa may be any amino acid
145 <400> SEQUENCE: 11
W--> 146     Arg Xaa Arg Ser
147         1
150 <210> SEQ ID NO: 12
151 <211> LENGTH: 15
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 12
156     Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His
157         1             5             10             15
160 <210> SEQ ID NO: 13
161 <211> LENGTH: 5
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Xaa may be any amino acid
168 <400> SEQUENCE: 13
W--> 169     Arg Xaa Arg Ser His
170         1             5
173 <210> SEQ ID NO: 14
174 <211> LENGTH: 269
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 14
179     Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
180         1             5             10             15
182     His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
183         20             25             30
185     Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
186         35             40             45
188     Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
189         50             55             60
191     Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
192         65             70             75             80
194     Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
195         85             90             95
197     Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
198         100            105            110
200     Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
201         115            120            125

```

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```

203      Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
204          130                      135                      140
206      Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
207          145                      150                      155                      160
209      Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu Asn Leu Asn Met
210                      165                      170                      175
212      Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
213          180                      185                      190
215      Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
216          195                      200                      205
218      Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
219          210                      215                      220
221      Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
222          225                      230                      235                      240
224      Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
225                      245                      250                      255
227      Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
228          260                      265
231 <210> SEQ ID NO: 15
232 <211> LENGTH: 7
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 15
237      Pro Glu Arg Ile Leu Ser Ile
238          1                      5
241 <210> SEQ ID NO: 16
242 <211> LENGTH: 9
243 <212> TYPE: PRT
244 <213> ORGANISM: Homo sapiens
246 <400> SEQUENCE: 16
247      Gly Gly Ser Arg Ala Arg Asn Leu Pro
248          1                      5
251 <210> SEQ ID NO: 17
252 <211> LENGTH: 463
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 17
257      Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
258          1                      5                      10                      15
260      Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
261          20                      25                      30
263      Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
264          35                      40                      45
266      Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
267          50                      55                      60
269      Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp
270          65                      70                      75                      80
272      Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
273          85                      90                      95

```

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```

275   Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
276               100               105               110
278   Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
279               115               120               125
281   Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
282               130               135               140
284   Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
285               145               150               155               160
287   Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
288               165               170               175
290   Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
291               180               185               190
293   Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
294               195               200               205
296   Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
297               210               215               220
299   Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
300               225               230               235               240
302   Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
303               245               250               255
305   Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
306               260               265               270
308   Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
309               275               280               285
311   Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
312               290               295               300
314   Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
315               305               310               315               320
317   Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
318               325               330               335
320   Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
321               340               345               350
323   Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
324               355               360               365
326   Tyr Asp Tyr Ser Tyr Ala Gly Arg Gly Ser Tyr Gly Asp Leu Gly
327               370               375               380
329   Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
330               385               390               395               400
332   Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
333               405               410               415
335   Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
336               420               425               430
338   Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
339               435               440               445
341   Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
342               450               455               460
345 <210> SEQ ID NO: 18
346 <211> LENGTH: 570
347 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/784,950

DATE: 03/04/2005
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Input Set : A:\ABXCBLCD147 CON sequence listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2
Seq#:13; Xaa Pos. 2
Seq#:23; Xaa Pos. 150
Seq#:30; Xaa Pos. 140
Seq#:31; Xaa Pos. 147,151
Seq#:62; N Pos. 234

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

VERIFICATION SUMMARY

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Input Set : A:\ABXCBLCD147 CON sequence listing.txt

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L:146 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:11
L:146 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:169 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
L:169 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:599 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:23
L:599 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:23
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:144
L:894 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:30
L:894 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:30
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:128
L:937 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:31
L:937 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:31
L:937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:144
L:1573 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:62
L:1573 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:62
L:1573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:180